RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____ 10/572, 696 _____

Source: _____ JFWP _____

Date Processed by STIC: _____ 03/29/2006 _____

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IFWP

RAW SEQUENCE LISTING   DATE: 03/29/2006
PATENT APPLICATION: US/10/572,696   TIME: 09:47:07

Input Set : **A:\42-000400us sequence final.ST25.txt**
Output Set: **N:\CRF4\03292006\J572696.raw**

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 3  <110> APPLICANT: Garvan Institute of Medical Research
 5  <120> TITLE OF INVENTION: Method of modulating bone growth, remodeling and adiposity
 7  <130> FILE REFERENCE: 42-000400US
C--> 9  <140> CURRENT APPLICATION NUMBER: US/10/572,696
C--> 9  <141> CURRENT FILING DATE: 2006-03-20
 9  <160> NUMBER OF SEQ ID NOS: 20
11  <170> SOFTWARE: PatentIn version 3.3
13  <210> SEQ ID NO: 1
14  <211> LENGTH: 1180
15  <212> TYPE: DNA
16  <213> ORGANISM: human neuropeptide Y1 receptor
19  <220> FEATURE:
20  <221> NAME/KEY: CDS
21  <222> LOCATION: (7)..(1161)
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24  aagctt atg aat tca aca tta ttt tcc cag gtt gaa aat cat tca gtc        48
25         Met Asn Ser Thr Leu Phe Ser Gln Val Glu Asn His Ser Val
26          1               5                  10
28  cac tct aat ttc tca gag aag aat gcc cag ctt ctg gct ttt gaa aat      96
29  His Ser Asn Phe Ser Glu Lys Asn Ala Gln Leu Leu Ala Phe Glu Asn
30  15                  20                  25                  30
32  gat gat tgt cat ctg ccc ttg gcc atg ata ttt acc tta gct ctt gct     144
33  Asp Asp Cys His Leu Pro Leu Ala Met Ile Phe Thr Leu Ala Leu Ala
34                  35                  40                  45
36  tat gga gct gtg atc att ctt ggt gtc tct gga aac ctg gcc ttg atc     192
37  Tyr Gly Ala Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile
38                  50                  55                  60
40  ata atc atc ttg aaa caa aag gag atg aga aat gtt acc aac atc ctg     240
41  Ile Ile Ile Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu
42          65                  70                  75
44  att gtg aac ctt tcc ttc tca gac ttg ctt gtt gcc atc atg tgt ctc     288
45  Ile Val Asn Leu Ser Phe Ser Asp Leu Leu Val Ala Ile Met Cys Leu
46          80                  85                  90
48  ccc ttt aca ttt gtc tac aca tta atg gac cac tgg gtc ttt ggt gag     336
49  Pro Phe Thr Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu
50  95                  100                 105                 110
52  gcg atg tgt aag ttg aat cct ttt gtg caa tgt gtt tca atc act gtg     384
53  Ala Met Cys Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val
54                  115                 120                 125
56  tcc att ttc tct ctg gtt ctc att gct gtg gaa cga cat cag ctg ata     432
57  Ser Ile Phe Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile
58                  130                 135                 140
60  atc aac cct cga ggg tgg aga cca aat aat aga cat gct tat gta ggt     480
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61 Ile Asn Pro Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Val Gly
62          145                 150                 155
64 att gct gtg att tgg gtc ctt gct gtg gct tct tct ttg cct ttc ctg     528
65 Ile Ala Val Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Leu
66      160                 165                 170
68 atc tac caa gta atg act gat gag ccg ttc caa aat gta aca ctt gat     576
69 Ile Tyr Gln Val Met Thr Asp Glu Pro Phe Gln Asn Val Thr Leu Asp
70 175                 180                 185                 190
72 gcg tac aaa gac aaa tac gtg tgc ttt gat caa ttt cca tcg gac tct     624
73 Ala Tyr Lys Asp Lys Tyr Val Cys Phe Asp Gln Phe Pro Ser Asp Ser
74              195                 200                 205
76 cat agg ttg tct tat acc act ctc ctc ttg gtg ctg cag tat ttt ggt     672
77 His Arg Leu Ser Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly
78              210                 215                 220
80 cca ctt tgt ttt ata ttt att tgc tac ttc aag ata tat ata cgc cta     720
81 Pro Leu Cys Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu
82          225                 230                 235
84 aaa agg aga aac aac atg atg gac aag atg aga gac aat aag tac agg     768
85 Lys Arg Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg
86      240                 245                 250
88 tcc agt gaa acc aaa aga atc aat atc atg ctg ctc tcc att gtg gta     816
89 Ser Ser Glu Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val Val
90 255                 260                 265                 270
92 gca ttt gca gtc tgc tgg ctc cct ctt acc atc ttt aac act gtg ttt     864
93 Ala Phe Ala Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val Phe
94              275                 280                 285
96 gat tgg aat cat cag atc att gct acc tgc aac cac aat ctg tta ttc     912
97 Asp Trp Asn His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe
98              290                 295                 300
100 ctg ctc tgc cac ctc aca gca atg ata tcc act tgt gtc aac ccc ata     960
101 Leu Leu Cys His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile
102          305                 310                 315
104 ttt tat ggg ttc ctg aac aaa aac ttc cag aga gac ttg cag ttc ttc     1008
105 Phe Tyr Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe
106      320                 325                 330
108 ttc aac ttt tgt gat ttc cgg tct cgg gat gat gat tat gaa aca ata     1056
109 Phe Asn Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile
110 335                 340                 345                 350
112 gcc atg tcc acg atg cac aca gat gtt tcc aaa act tct ttg aag caa     1104
113 Ala Met Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln
114              355                 360                 365
116 gca agc cca gtc gca ttt aaa aaa atc aac aac aat gat gat aat gaa     1152
117 Ala Ser Pro Val Ala Phe Lys Lys Ile Asn Asn Asn Asp Asp Asn Glu
118              370                 375                 380
120 aaa atc tga aactacttat agctctaga                                   1180
121 Lys Ile
125 <210> SEQ ID NO: 2
126 <211> LENGTH: 384
127 <212> TYPE: PRT
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RAW SEQUENCE LISTING   DATE: 03/29/2006
PATENT APPLICATION: US/10/572,696   TIME: 09:47:07

Input Set : A:\42-000400us sequence final.ST25.txt
Output Set: N:\CRF4\03292006\J572696.raw

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128 <213> ORGANISM: human neuropeptide Y1 receptor
130 <400> SEQUENCE: 2
132 Met Asn Ser Thr Leu Phe Ser Gln Val Glu Asn His Ser Val His Ser
133 1             5                   10                  15
136 Asn Phe Ser Glu Lys Asn Ala Gln Leu Leu Ala Phe Glu Asn Asp Asp
137             20                  25                  30
140 Cys His Leu Pro Leu Ala Met Ile Phe Thr Leu Ala Leu Ala Tyr Gly
141             35                  40                  45
144 Ala Val Ile Ile Leu Gly Val Ser Gly Asn Leu Ala Leu Ile Ile Ile
145     50                  55                  60
148 Ile Leu Lys Gln Lys Glu Met Arg Asn Val Thr Asn Ile Leu Ile Val
149 65                  70                  75                  80
152 Asn Leu Ser Phe Ser Asp Leu Leu Val Ala Ile Met Cys Leu Pro Phe
153             85                  90                  95
156 Thr Phe Val Tyr Thr Leu Met Asp His Trp Val Phe Gly Glu Ala Met
157             100                 105                 110
160 Cys Lys Leu Asn Pro Phe Val Gln Cys Val Ser Ile Thr Val Ser Ile
161             115                 120                 125
164 Phe Ser Leu Val Leu Ile Ala Val Glu Arg His Gln Leu Ile Ile Asn
165     130                 135                 140
168 Pro Arg Gly Trp Arg Pro Asn Asn Arg His Ala Tyr Val Gly Ile Ala
169 145                 150                 155                 160
172 Val Ile Trp Val Leu Ala Val Ala Ser Ser Leu Pro Phe Leu Ile Tyr
173             165                 170                 175
176 Gln Val Met Thr Asp Glu Pro Phe Gln Asn Val Thr Leu Asp Ala Tyr
177             180                 185                 190
180 Lys Asp Lys Tyr Val Cys Phe Asp Gln Phe Pro Ser Asp Ser His Arg
181             195                 200                 205
184 Leu Ser Tyr Thr Thr Leu Leu Leu Val Leu Gln Tyr Phe Gly Pro Leu
185     210                 215                 220
188 Cys Phe Ile Phe Ile Cys Tyr Phe Lys Ile Tyr Ile Arg Leu Lys Arg
189 225                 230                 235                 240
192 Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser
193             245                 250                 255
196 Glu Thr Lys Arg Ile Asn Ile Met Leu Leu Ser Ile Val Val Ala Phe
197             260                 265                 270
200 Ala Val Cys Trp Leu Pro Leu Thr Ile Phe Asn Thr Val Phe Asp Trp
201             275                 280                 285
204 Asn His Gln Ile Ile Ala Thr Cys Asn His Asn Leu Leu Phe Leu Leu
205     290                 295                 300
208 Cys His Leu Thr Ala Met Ile Ser Thr Cys Val Asn Pro Ile Phe Tyr
209 305                 310                 315                 320
212 Gly Phe Leu Asn Lys Asn Phe Gln Arg Asp Leu Gln Phe Phe Phe Asn
213             325                 330                 335
216 Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met
217             340                 345                 350
220 Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser
221             355                 360                 365
224 Pro Val Ala Phe Lys Lys Ile Asn Asn Asn Asp Asp Asn Glu Lys Ile
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225     370                 375                 380
228 <210> SEQ ID NO: 3
229 <211> LENGTH: 3747
230 <212> TYPE: DNA
231 <213> ORGANISM: human neuropeptide Y2 receptor
234 <220> FEATURE:
235 <221> NAME/KEY: CDS
236 <222> LOCATION: (496)..(1638)
238 <400> SEQUENCE: 3
239 gaattcggcc gctgagagac cctggacact gttcctgctc cctcgccacc aaaacttctc      60
241 ctccagtccc ctccctgca ggaccatcgc ccgcagcctc tgcacctgtt ttcttgtgtt     120
243 taagggtggg gtttgccccc ctccccacgc tcccatctct gatcctccca ccttcacccg     180
245 cccacccccgc gagtgagtgc ggtgcccagg cgcgcttggc ctgagaggtc ggcagcagac     240
247 ccggcagcgc caaccgccca gccgctctga ctgctccggc tgcccgcccg cgcggcgcgg     300
249 gctgtcctgg accctaggag gggacggaac cggacttgcc tttgggcacc ttccagggcc     360
251 ctctccaggt cggctggcta atcatcggac agacggactg cacacatctt gtttccgcgt     420
253 ctccgcaaaa acgcgaggtc caggtcagtt gtagactctt gtgctggttg caggccaagt     480
255 ggacctgtac tgaaa atg ggt cca ata ggt gca gag gct gat gag aac cag     531
256                Met Gly Pro Ile Gly Ala Glu Ala Asp Glu Asn Gln
257                  1               5                  10
259 aca gtg gaa gaa atg aag gtg gaa caa tac ggg cca caa aca act cct     579
260 Thr Val Glu Glu Met Lys Val Glu Gln Tyr Gly Pro Gln Thr Thr Pro
261          15                  20                  25
263 aga ggt gaa ctg gtc cct gac cct gag cca gag ctt ata gat agt acc     627
264 Arg Gly Glu Leu Val Pro Asp Pro Glu Pro Glu Leu Ile Asp Ser Thr
265      30                  35                  40
267 aag ctg att gag gta caa gtt gtt ctc ata ttg gcc tac tgc tcc atc     675
268 Lys Leu Ile Glu Val Gln Val Val Leu Ile Leu Ala Tyr Cys Ser Ile
269 45                  50                  55                  60
271 atc ttg ctt ggg gta att ggc aac tcc ttg gtg atc cat gtg gtg atc     723
272 Ile Leu Leu Gly Val Ile Gly Asn Ser Leu Val Ile His Val Val Ile
273              65                  70                  75
275 aaa ttc aag agc atg cgc aca gta acc aac ttt ttc att gcc aat ctg     771
276 Lys Phe Lys Ser Met Arg Thr Val Thr Asn Phe Phe Ile Ala Asn Leu
277          80                  85                  90
279 gct gtg gca gat ctt ttg gtg aac act ctg tgt cta ccg ttc act ctt     819
280 Ala Val Ala Asp Leu Leu Val Asn Thr Leu Cys Leu Pro Phe Thr Leu
281          95                  100                 105
283 acc tat acc tta atg ggg gag tgg aaa atg ggt cct gtc ctg tgc cac     867
284 Thr Tyr Thr Leu Met Gly Glu Trp Lys Met Gly Pro Val Leu Cys His
285      110                 115                 120
287 ctg gtg ccc tat gcc cag ggc ctg gca gta caa gta tcc aca atc acc     915
288 Leu Val Pro Tyr Ala Gln Gly Leu Ala Val Gln Val Ser Thr Ile Thr
289 125                 130                 135                 140
291 ttg aca gta att gcc ctg gac cgg cac agg tgc atc gtc tac cac cta     963
292 Leu Thr Val Ile Ala Leu Asp Arg His Arg Cys Ile Val Tyr His Leu
293              145                 150                 155
295 gag agc aag atc tcc aag cga atc agc ttc ctg att att ggc ttg gcc    1011
296 Glu Ser Lys Ile Ser Lys Arg Ile Ser Phe Leu Ile Ile Gly Leu Ala
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RAW SEQUENCE LISTING   DATE: 03/29/2006
PATENT APPLICATION: US/10/572,696   TIME: 09:47:07

Input Set : A:\42-000400us sequence final.ST25.txt
Output Set: N:\CRF4\03292006\J572696.raw

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297              160              165              170
299 tgg ggc atc agt gcc ctg ctg gca agt ccc ctg gcc atc ttc cgg gag   1059
300 Trp Gly Ile Ser Ala Leu Leu Ala Ser Pro Leu Ala Ile Phe Arg Glu
301         175              180              185
303 tat tcg ctg att gag atc att ccg gac ttt gag att gtg gcc tgt act   1107
304 Tyr Ser Leu Ile Glu Ile Ile Pro Asp Phe Glu Ile Val Ala Cys Thr
305     190              195              200
307 gaa aag tgg cct ggc gag gag aag agc atc tat ggc act gtc tat agt   1155
308 Glu Lys Trp Pro Gly Glu Glu Lys Ser Ile Tyr Gly Thr Val Tyr Ser
309 205              210              215              220
311 ctt tct tcc ttg ttg atc ttg tat gtt ttg cct ctg ggc att ata tca   1203
312 Leu Ser Ser Leu Leu Ile Leu Tyr Val Leu Pro Leu Gly Ile Ile Ser
313             225              230              235
315 ttt tcc tac act cgc att tgg agt aaa ttg aag aac cat gtc agt cct   1251
316 Phe Ser Tyr Thr Arg Ile Trp Ser Lys Leu Lys Asn His Val Ser Pro
317             240              245              250
319 gga gct gca aat gac cac tac cat cag cga agg caa aaa acc acc aaa   1299
320 Gly Ala Ala Asn Asp His Tyr His Gln Arg Arg Gln Lys Thr Thr Lys
321             255              260              265
323 atg ctg gtg tgt gtg gtg gtg gtg ttt gcg gtc agc tgg ctg cct ctc   1347
324 Met Leu Val Cys Val Val Val Val Phe Ala Val Ser Trp Leu Pro Leu
325     270              275              280
327 cat gcc ttc cag ctt gcc gtt gac att gac agc cag gtc ctg gac ctg   1395
328 His Ala Phe Gln Leu Ala Val Asp Ile Asp Ser Gln Val Leu Asp Leu
329 285              290              295              300
331 aag gag tac aaa ctc atc ttc aca gtg ttc cac att atc gcc atg tgc   1443
332 Lys Glu Tyr Lys Leu Ile Phe Thr Val Phe His Ile Ile Ala Met Cys
333             305              310              315
335 tcc act ttt gcc aat ccc ctt ctc tat ggc tgg atg aac agc aac tac   1491
336 Ser Thr Phe Ala Asn Pro Leu Leu Tyr Gly Trp Met Asn Ser Asn Tyr
337             320              325              330
339 aga aag gct ttc ctc tcg gcc ttc cgc tgt gag cag cgg ttg gat gcc   1539
340 Arg Lys Ala Phe Leu Ser Ala Phe Arg Cys Glu Gln Arg Leu Asp Ala
341             335              340              345
343 att cac tct gag gtg tcc gtg aca ttc aag gct aaa aag aac ctg gag   1587
344 Ile His Ser Glu Val Ser Val Thr Phe Lys Ala Lys Lys Asn Leu Glu
345     350              355              360
347 gtc aga aag aac agt ggc ccc aat gac tct ttc aca gag gct acc aat   1635
348 Val Arg Lys Asn Ser Gly Pro Asn Asp Ser Phe Thr Glu Ala Thr Asn
349 365              370              375              380
351 gtc taaggaagct gtggtgtgaa aatgtatgga tgaattctga ccagagctat   1688
352 Val
355 gaatctggtt gatggcggct cacaagtgaa aactgatttc cattttaaa gaagaagtgg   1748
357 atctaaatgg aagcatctgc tgtttaattc ctggaaaact ggctgggcag agcctgtgtg   1808
359 aaaatactgg aattcaaaga taaggcaaca aaatggttta cttaacagtt ggttgggtag   1868
361 taggttgcat tatgagtaaa agcagagaga agtactttg attattttcc tggagtgaag   1928
363 aaaacttgaa caagaaattg gtattatcaa agcattgctg agagacggtg ggaaaataag   1988
365 ttgactttca aatcacgtta ggacctggat tgaggaggtg tgcagttcgc tgctccctgc   2048
367 ttggcttatg aaaacaccac tgaacagaaa tttctccagg gagccacagg ctctccttca   2108
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VERIFICATION SUMMARY   DATE: 03/29/2006
PATENT APPLICATION: **US/10/572,696**   TIME: 09:47:08

Input Set : **A:\42-000400us sequence final.ST25.txt**
Output Set: **N:\CRF4\03292006\J572696.raw**

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date